

## Mapping migration in a songbird using high-resolution genetic markers

Kristen Ruegg<sup>1,2</sup>, Eric C. Anderson<sup>3,4</sup>, Kristina L. Paxton<sup>5,6</sup>, Vanessa Apkenas<sup>3</sup>, Sirena Lao<sup>1</sup>, Rodney B. Siegel<sup>7</sup>, David F. DeSante<sup>7</sup>, Frank Moore<sup>6</sup> and Thomas B. Smith<sup>1,8</sup>

### ***METHODS SUPPLEMENT***

**(a) RAD-PE library preparation.** In short, 100ng of genomic DNA from each individual was digested with 2 U of *SbfI*-HF enzyme (New England Biolabs, Beverly MA, USA) for 60 min at 37° C. The reactions were then inactivated by holding at 65° C for 20 min. The P1 adapter (a modified Illumina adapter, see Baird *et al.* (1)) was ligated to the products of the restriction reactions, and the "barcoding" of the various samples was achieved with a set of index nucleotides within the P1 adapter sequence. 1 µL of 100 nM P1 adapter was then added to each sample with 60 U T4 DNA Ligase (Enzymatics, Inc.). Reactions were incubated at room temperature for 1 hour and then heat-inactivated by holding at 65° C for 10 min. The reactions were then pooled and the products were randomly sheared to a mean size of 500 bp using a Bioruptor NGS (Diagenode). The material was electrophoresed through a 1.5% agarose gel and DNA in the range of 200-700 bp was isolated using a MinElute Gel Extraction Kit (Qiagen). To remove overhangs, ssDNA ends were treated with 1 µL High Concentration End-Repair Mix (Enzymatics, Inc.). The samples were then purified by passing through a MinElute column (Qiagen) and 3'-adenine overhangs were added by the addition of 50 U Klenow (3'-5' exo-) (Enzymatics) and 1 µL 10mM dATP. Samples were then incubation at 37° C for 30 min. Following re-purification, 1 µL of 1 µM P2 adapter (a modified Illumina adapter, see Baird *et al.* (1)) was ligated with 600 U T4 DNA Ligase (Enzymatics, Inc.) for 1 hour at room

temperature. The samples were then purified as above and eluted in a volume of 15  $\mu\text{L}$ . Following quantification using a Qubit fluorimeter (Invitrogen), 10 ng was taken as the template for a 100  $\mu\text{L}$  PCR containing 50  $\mu\text{L}$  Phusion Master Mix (NEB), 5  $\mu\text{L}$  10  $\mu\text{M}$  P1 amplification primer and 5  $\mu\text{L}$  10  $\mu\text{M}$  P2 amplification primer. The Phusion PCR settings followed standard protocols (NEB) over 18 cycles. Amplicons were then gel purified, the size range 300-700 bp was excised from the gel and its DNA content adjusted to 3.6 ng/ $\mu\text{L}$ .

***(b) Pre-amplification and final SNPtype Assay amplification protocol.*** All protocols and genotyping efforts were carried out with the use of Fluidigm Corporation SNPtype™ Assays designed for 96.96 Dynamic Genotyping Arrays™ on an EP1™ Genotyping System. This platform enabled us to efficiently genotype 96 SNP loci in 94 individuals at a time with two non-template controls per run. An initial pre-amplification step was performed on genomic DNA using a primer pool containing 96 unlabeled locus specific SNPtype primers (Specific Target Amplification (STA) and Locus Specific Primer (LSP) assays) made up ahead of time according to the following parameters: 2  $\mu\text{L}$  100  $\mu\text{M}$  STA primer for each of 96 assays, 2  $\mu\text{L}$  100  $\mu\text{M}$  LSP primer for each of 96 assays, 16  $\mu\text{L}$  5  $\mu\text{M}$  Tris dH<sub>2</sub>O. PCR master mix was comprised of: 2.6  $\mu\text{L}$  Qiagen® 2X Multiplex PCR Master Mix, 0.52  $\mu\text{L}$  primer pool, 0.78  $\mu\text{L}$  dH<sub>2</sub>O. Pre-amplification thermal cycling conditions were as follows: an initial denaturation of 15 min at 95 °C, then [15 s at 95 °C and 4 min at 60 °C] x 14 and a final hold at 10 °C. Products were then diluted 1:100 with 2 uM Tris dH<sub>2</sub>O. We ran samples as: 2.5  $\mu\text{L}$  diluted DNA, 3  $\mu\text{L}$  Biotium Fast Probe qPCR Master Mix, 0.3  $\mu\text{L}$  SNPtype 20X Sample Loading Reagent, 0.1  $\mu\text{L}$  60X SNPtype reagent,

0.036 µl ROX™ Passive Reference Dye, 0.064 µl dH<sub>2</sub>O. Assays were ran as: 1 µl SNPtype assay mix (Allele Specific Primer (ASP) and LSP assays), 2.5 µl 2X Assay Loading Reagent, 1.5 µl dH<sub>2</sub>O. Once loaded into the array, samples and assays went through another amplification step in order to detect SNP-specific alleles: a thermal mix step of [30 min at 70 °C and 10 min at 25 °C], initial denaturation of 5 min at 95 °C, [95 °C for 15 s, 63 °C for 45 s, 72 °C for 15 s] x 3 (-1 °C/cycle), [95 °C for 15 s, 60 °C for 45 s, 72 °C for 15 s] x 34 and a final cooling step of 25 °C for 10 s. We imaged results and called alleles with Fluidigm Genotyping Analysis Software.

### **Figure Legend**

**SI Figure 1.** Results of the population genetic analysis for Wilson's warblers across the breeding range using STRUCTURE. These data depict the output from all 10 runs at each K value (K= 1-9) and the data are plotted using the program Distruct.

**SI Table 1.** RAD sequencing results for SNP ascertainment panel. For each individual, the population, the subspecies, the library prep pool ("pool"), the number of Illumina sequencing reads attained for the sample ("N reads"), the number of unique RADtags with between 5x and 100x coverage ("N RADtags"), the median depth of sequencing coverage for the sample across all RADtags ("Med. seq. depth"), and the mean quality score per pool ("Mean Quality Score") are indicated.

Individual	Population	Subspecies	Pool	N reads	N RADtags	Med seq. depth	Mean Quality Score
QUE_98N2036	Lac St. Jean, Quebec	<i>W. c. pusilia</i>	<i>C</i>	7,551,325	168,880	28	35
QUE_98N2038	Lac St. Jean, Quebec	<i>W. c. pusilia</i>	<i>C</i>	9,621,485	178,891	35	35
QUE_98N2040	Lac St. Jean, Quebec	<i>W. c. pusilia</i>	<i>C</i>	9,295,065	172,704	35	35
QUE_98N2043	Lac St. Jean, Quebec	<i>W. c. pusilia</i>	<i>C</i>	9,488,049	176,141	35	35
QUE_98N2044	Lac St. Jean, Quebec	<i>W. c. pusilia</i>	<i>C</i>	8,713,916	173,084	32	35
AB_03N2126	Cochran, Alberta	<i>W. c. pusilia</i> / <i>W. c. pileolata</i>	<i>D</i>	6,938,762	158,537	27	35
AB_03N2127	Cochran, Alberta	<i>W. c. pusilia</i> / <i>W. c. pileolata</i>	<i>D</i>	8,761,518	175,795	30	35
AB_03N2128	Cochran, Alberta	<i>W. c. pusilia</i> / <i>W. c. pileolata</i>	<i>D</i>	8,901,837	178,996	30	35
AB_03N2182	Cochran, Alberta	<i>W. c. pusilia</i> / <i>W. c. pileolata</i>	<i>D</i>	6,551,410	159,025	25	35
AB_03N2185	Cochran, Alberta	<i>W. c. pusilia</i> / <i>W. c. pileolata</i>	<i>D</i>	7,230,512	164,589	27	35
AK_97N4037	Juneau, AK	<i>W. c. pileolata</i>	<i>D</i>	8,829,749	174,495	32	35
AK_97N4039	Juneau, AK	<i>W. c. pileolata</i>	<i>D</i>	9,222,262	176,075	33	35
AK_97N4046	Juneau, AK	<i>W. c. pileolata</i>	<i>D</i>	8,826,285	173,830	32	35
AK_97N4049	Juneau, AK	<i>W. c. pileolata</i>	<i>D</i>	8,899,908	172,830	33	35
AK_97N4059	Juneau, AK	<i>W. c. pileolata</i>	<i>D</i>	5,574,860	161,879	22	35
06N26537	Cibola, AZ	<i>W. c. pileolata</i>	<i>E</i>	15,425,338	336,924	26	35
96N2356	Lake Tahoe, CA	<i>W. c. chryseola</i>	<i>E</i>	15,955,805	340,694	27	35
PRBO_08	Point Reyes, CA	<i>W. c. chryseola</i>	<i>E</i>	6,302,518	154,403	25	35
PRBO_11	Point Reyes, CA	<i>W. c. chryseola</i>	<i>E</i>	18,699,537	204,819	56	35
PRBO_19	Point Reyes, CA	<i>W. c. chryseola</i>	<i>E</i>	20,436,772	212,079	57	35
PRBO_20	Point Reyes, CA	<i>W. c. chryseola</i>	<i>E</i>	16,037,892	197,870	48	35
PRBO_25	Point Reyes, CA	<i>W. c. chryseola</i>	<i>E</i>	7,503,722	164,383	28	35

SI Table 2. SNPType Assay information.

Assay Name	Chromosome	Zebra Finch Genome Coordinates	SNP Frequency in Southwest (SW)	SNP Frequency in Alberta (AB)	SNP Frequency in Alaska (AK)	SNP Frequency in California (PRBO)	SNP Frequency in Quebec (QUE)	Total Number of Genotypes in each population (SW, AB, AK, PRBO, QUE)	AssaySequence	Contig Length (bp)	Average depth of sequencing across the contig within an individual	Total depth of sequence at SNP locus across all individuals
AB_AK_02	8	3027501	1	0.25	0.9	0.75	0	2 4 5 4 5	GCCATAACTATGAAGTGCCCTAGTTTTGGCTTTGAT ATGACTGAGTTGTGAGCCTCAGAAAAATGTTCTC AGC[A/G]TGCACTCCAGGGTGTGTTCTTCTCTCAA AGCTGCTGAAATGCGCAGCAGAGGATTACTGT GAGCAACTGA	240	28.08	1133
AB_AK_03	3	22026684	0.25	0.125	0.75	0.4	0	2 4 4 5 5	TGCTGAAATCTACTAATTAATTCACATTCAAACACC CATAAAGACACACCTCATCTGACCAGATGAAATCT CA[T/C]GGCTAGCATTGCTATTGTGCAGAGGAAAG CAACTTCCAAATTGTCACGCTCTCTCCAACAGTGGT TCCTTCCC	373	32.91	929
AB_AK_04	14	16110885	0.75	1	0.375	0.5	1	2 4 4 5 5	CAGACATCCAGACTCGGTGTCACTCCGGCATCTCA TCAAACAGGAAATGCTTTTCCAGGGTCATCTGGGA TCT[C/G]GGCAGCACTGCTGCTCATCAGCATAATA ATGGCAGCTGAACGATGCTTGGCAGAGAGGGGC ACCTCTGCACA	381	18.93	745
AB_AK_05	NA	NA	1	1	0.375	0.5	0	1 5 4 4 5	TGGAGCACCCTCCACCCCTCTTTCATAGCTTTGATG ACTGCAGAGTTGTTCCTCTCATCTGTCTCACTCTC T[T/C]CTCACAAGAGCTGCACAGTTTACTCTTGG ATATGTTATCCAGAGATGCTACTACCATCAAGT TCATCTC	296	19.50	1086
AB_AK_06	NA	NA	0.25	0	0.625	0.5	0.125	2 4 4 4 4	AATCTAAAAGAAAAAATATGGATTTCACATCTAGG AAAACCCAAACCAACCAAAAGGCCATGTAGGC TAGG[A/G]CACCTCAAGTGTGTGAGAGGTGCTGCT GCCAGAGTGCACTCTGGTCCCACTCCCTGGAACA GGGACAGAGATG	329	36.57	1150
AB_AK_08	1	52827600	0.5	0	0.5	0.5	0.5	2 4 4 5 5	GAACAGGGTAATTACTCTGTGAGAGAAGAGCTTC CAGGAGGTGCTGAGAAGTGTAATTCATGTACAGA AAAAG[A/G]TTTTCAGACAAAAATAAAGCATCTG TAAGGACAAAGTAGTAGTGAAGTGATGGATGTCCAG ACATACATATGTA	462	24.68	893
AB_AK_09	2	18244201	1	1	0.5	0.8	1	2 4 4 5 5	CCACACCTCACTATTGTTACTAAAGTCAGCTGGACA CTCCTCTGTCTCCACGTGCCCACTCAACTCTTTGC TT[G/C]TGTGTGGATGAAGGAGGGAAGACAGGATC TGGCTGAGTGTGGGGCTCTTCTCATCATCTTAAA GAGGATGCAA	362	33.73	449
AB_AK_11	7	5412014	0	1	0.5	0.875	1	1 4 4 4 5	TTTTTCGATAGGCTTTAATAGTTTAATTTAACAGTC TTAAACACGCTCTATATTAAGTCTGAGACATAATGTGAT T[T/A]GAGATTGAGCAGCTGCATGGCACAAAAATA TATTTCACATTTTATTGTCTTTTATGCGGAAAAA GCTGAAA	279	17.06	234
AB_AK_12	NA	NA	1	1	0.5	0.7	0.125	2 5 4 5 4	CACCTCTTCCAAGACCTTTGGGAGGTCTCCAGCA AGGTGAGAGAGCACAGGGAACCTTCCAGCCACAGA CAGA[G/C]ACTGCTGAAGTGCAGGGAAGGTCT CACCTCTTTGACCCAGCAGGCAACCTGGGAGCCT GGGCAGAGGCAA	461	30.46	708
AB_AK_13	NA	NA	0.5	1	0.5	0.625	1	2 5 4 4 5	TGTCAGGTACTCTCTCCACAGCTATGCCTCCCTTGC ATCTACAAACCTGATGCTTGACCCCTCTGCATGTGA AA[C/T]JAGAAATTTTCTTCTCCACACTTCCGGCAT AGCCACTACAAGGATTATAGATGGATGCATCTTT CTTCAGAG	355	17.11	1026
AB_AK_15	1	93984316	0.25	0.5	1	1	1	2 5 5 4 5	CCCCAAGTCTGCTGTTGATATCTGTGGGGTCTTTA TGGAAGTTCCTTTAAGAAAGTCATCTAGGATTAA GG[A/T]JGGAAGCTGCTGAGCTACTTCATGTGGCTG AGTGGCACCAAGGAGCAGCAAGCCCTGTGCCAGGG ACAGAGATGT	248	31.31	822
AB_AK_20	1A	60531085	1	0.6	1	1	0.6	2 5 4 5 5	CTGCTGTATATCTCTCTGCTACAAATATAGAAAGTG ACTTTTTGAGGTTGCAGAGCAGTATCACTGTGCATG CTG[T/G]ATGTGCAAGATAAGCTGCCTTAGCTGGT GCTGGATGGACACTGCTAGCAAAGTTTATCTTTTA CTGGAGGACT	300	26.97	839
AB_AK_23	NA	NA	1	1	0.6	1	1	2 4 5 5 5	TCAGGGTATTATATAAGGAGGTTACACAAGCAGG ACTGTTCCGGGTTTATGAAGGGCCACCCAGCCTG GGCG[C/A]JAGAGGATGGACAGTGGGACGGGCAG CGGAACAGCGCTGCCGCTCGGACCTGGGGTCACA GTGAGACTGGGATG	237	22.41	528
AB_AK_24	NA	NA	0.75	0.5	0	0.375	1	2 5 4 4 5	AAGGCTAAGGATTCTCTGGGGGAGTCTCAGCA GCACACCACTCCATCTGTCCAGAGGGGCCCTCTG CCA[G/A]CCTACCATGTCCCTCTGTGCGAGTGCAA CCAAGCTCTCACCTCATGCTCCAGGGACACTCC ATCACATGGGG	433	39.49	1023
AB_AK_26	NA	NA	0.75	0.5	1	1	0.7	2 4 4 4 5	CCCAAGGGGATCATCCGAGAGCTCGGATTCTCGG ACAAGCCAATGGAAGACTCTTGAGTGCTTTATAC CGCCT[C/G]GAGGATCAGGCCATTGCCTCGCTCGTG TCTCTGGCTTCTCCAGACAAAACCTCTCTCTC TGAGCGCTCC	242	19.70	457
AB_AK_28	NA	NA	0.25	0.6	1	0.6	0.9	2 5 5 5 5	AAGAGTAAATAGTATTTCCATATGACATTGCAAGG CAAAGTTTGAACCTTTTGAAGTAAATTACCAAGGAT AGC[T/A]GCTGGAATAGGAGGATTATAGCCCAAC AGAGAAATGGGAATCCCTCATGAAGTGCAAGGTG GCAGGGTAGAGA	285	8.94	307
AB_AK_29	NA	NA	1	0.6	1	0.9	0.375	2 5 4 5 4	GATAATTTTTTGTGATTCTGCAGTTGTGGAAAA CAACTAGAAAAATAAACTCCAAGGATTATTTTC AA[G/A]CACTGTGATTTTGTATATAGAGGGGTGA TGACCTCATCCCTAGTTTATAATCTGTGACAAAGAT GTAAGAAT	384	45.25	1056

AB_AK_30	NA	NA	0.5	1	0.6	0.9	1	2 4 5 5	AGGTGAGGCTGCCAGGGCTGTAACACAAACCTGCG TCCTCCCTGCTGCTGAGGTGGAGTGTCTCAGCC AAGA[C/T]TGGAGGCAGGAGTGGGATTCATTGGC TGTGGGAAGCAAAAGGAGTCAAATTGCTCAGGGAAT CAGAGGCTCTACA	200	25.49	526
AB_AK_32	NA	NA	1	1	0.6	0.6	1	1 5 5 5	CCACACACTTCTTGGCCTTGGTCAATTGTACTATCA ATTGCCTTATACTGTGGAGCAAAAAATGTCACAGCT TA[A/G]AACACAGGTGAGTCTTGAATGCTGATGG ATTAGCAGAAAGGATATTGCTCAGGCTGAATAAGC ATCACTGTCT	303	17.03	270
AB_PRBO_01	NA	NA	0.5	0.125	0.625	0.9	1	2 4 4 5	GCCCCATTCAACCACTGAATATGACAAAGGCTTA GTTTATTATTGGAATTTCTCATTTACCCACAAGCAC TGT[C]AATATCTGATGCAATAAAAGCAGTCAGAA TGCAATCTGTAGCATCTCTAATCTGTAACGTGTTTA AACTGGGG	371	17.33	450
AB_PRBO_03	5	7709232	0	0	0.3	0.7	0	2 4 5 5	AAATCCATTTTAAAGAAAAAGCCATAATATAAAAC AAGCAGGGCTAGAGGCCAACCAATGGCTGATT GAGA[C/T]GGCAAATCTGAAGCTACTTCTATACGT ATTTGGAAGCTGGGAAGCTGCAATTTAGTATAGTA CAGCTACATCT	179	28.34	756
AB_PRBO_04	Z	64567518	0.25	0.3	0.5	1	1	2 5 5 5	CAGGTCCCAGGGGACCTTGACACAATTCAGCGGG CTGATGCAAACTCTCATGAAATTCATATGTGAAGT GCAA[G/A]GTCTACACTGGGTCTGGCAGATCTCA GGCTACAGTTGGGTGGAGAGGTGTGAGAGCAGC CCTGCAGAGAAAT	191	52.75	1426
AB_PRBO_05	NA	NA	0.5	0.125	0.6	0.8	0	2 4 5 4	GGTTTAAGCAAACTCTGTGAGGGCCATCTTAA CTGTCTGGGGAGATGTGCCCTCTATTGTGAGTGT TCT[G/A]CTCTGGGCTTCCGTTCCCTGTGTAGATAA ATTAGGCGTGTGGTCAGCTGGACAAAAATGAGA GAAACACCAC	435	49.91	464
AB_PRBO_06	1A	66726170	1	0.25	0.6	0.9	0	2 4 5 5	TCTGCCAGTCTCTGCTCCAAATGCTCTACTGAC CAATTCCAAATCTCTCAGGCAGAAAGGGGCCGA GTC[A/T]GTGGGAGCTGAGGGAAGCAGGAGCAGT GGAAACAAAGGCAGCAGC	191	8.28	926
AB_PRBO_07	5	7708797	0	0	0.25	0.625	0	2 5 4 5	TTAAAGGAGTGTGGGAAAGGAGGCAGGGCTGC GCCTCCACACTGTGTTGTACCAAGCTACAGAGCCA CTGCTT[C]TCCCTGGGAAGGTCCAAGCTCTAGCA CCACAGCTGCTCAAATCCATCCCCGAGCCCTCTGCC CAGCAGGGAGG	376	33.32	1242
AB_PRBO_08	12	10079166	0.75	0.375	0.6	1	0	2 4 5 5	TTAAATCCTGATCACCTCAGAGCTATGCTGCTG TCTCACTGACATGCTGTGTGGGAGAGGCAGAGTAC CAG[A/G]CAGACAGTACAGCCTTGCAAGCAAAA GACATTTGTGTGAGGCTGACAGTACAGCTGTTTCC TCTGTTGTAAC	329	25.71	926
AB_PRBO_09	NA	NA	0.75	0.375	1	1	0	2 4 5 5	AATATTGTTATAGATGACATGGATGGGATGGAATC TTTCATTAGTAAATTTGAAGACGCACCTAAGCTGGG AGCT[C]TGTGTTGATCTATTGGAAGGAGGATGGC TCTGCAGAGACATAGATCAGATGGATGGATGGG CAGAGTCCAAC	382	82.54	2923
AB_PRBO_10	NA	NA	1	1	1	0.375	0.875	1 5 4 4	ACCCATTATGCAATTTGGGGTGTACCTTGTGCTTC ATGCTTTACAGCATCTGTGCAACAGGGCTCTGATC CAC[G/A]AAGAAAACTCTAGATTCAAAATAATAGC TGTTGTCAATTGAAGCTTTCCCTCAGGAGGTGAAC CACAGAAATT	255	21.71	598
AB_PRBO_11	Z	31039342	0.5	1	1	0.375	1	2 5 5 4	GAAAAATGTAAGTGATGATTATCAAAAGCAGATG AATAATTTCTTAATGAGAAAAATATACAGCAGAAATA ATCT[A/G]TTTTCTTCAATAATAGACTGACTTACAG GTTTATCAATCTTGTCTTCTGACAAGTGATTTAGA AAAAAATTG	190	14.04	479
AB_PRBO_13	1A	48408035	0.75	1	0.9	0.4	0.2	2 5 5 5	AGACCTAAAAATGCTAAGACAGGATGTAAATACC TTATTGCATCACTGGTCAAGGCAAGCCCTGCAGTC CCCT[C/G]TTTTATCTTAAATGATAAAGCTTTATTG CCAGTCAATAAAATGCAGTGTGCTAAACCCACGTT ATTTAGCATA	391	19.72	792
AB_PRBO_14	NA	NA	0.5	0	0	0.6	0	2 5 5 4	TTAAAGCATCAAAAGGTGGGAGATTTAGTTGGC TCTGTCTAGGCAGGCAGAGAGGCATCTTCAGGACT ACAAA[A/G]CAGTGAGCCAGGTGCACAGCAGCCAG TGCCCTGCAGCCTGGCACAGTCTTTCAGGGGCGAG	187	51.61	1175
AB_PRBO_15	9	15661046	0.25	0.25	0.3	0.8	1	2 4 5 5	GGGCATGAGGTAAGAAGATTGTAGAGCATAGG AGACTTTCTTTTCCATCTGTGTGATGAGTTGATAGC ATGA[C/T]GTCTCTCTTCCATGGCCAGACCTGGCTC CAGGCAGGAGAAAAAGGTCTCCTTCACTGGGCACGG CAGGGAGACAT	390	19.91	1074
AB_PRBO_17	2	46885560	0.5	1	0.9	0.5	0	1 5 5 5	TCTTAATGCATATGCTGTACATAGTAGGTTCAAAG CTTAGTGTGGTCCAAACAGATGAAAAACACTACCT TAA[T/C]CATGCAATTACAGAAGCTCTGTAAACTG ACCTATGGAATAACATGCAAGACTCTGGTGAATGT AATACAAA	333	16.47	673
AB_PRBO_19	NA	NA	0.25	0	0.2	0.5	0	2 5 5 4	TTCCCCCTCAAGCACTAAATTTCAAATGCAGAGT CTAAGTCCTTCTACAACAGATTGTCAATCTAATAAT CA[G/A]CTGTACAGTAATTAGATAGAGCTCCAAGC TTCAGTATTGTCTATGTCTGAGACTCAGGTGGTAT TGATGAGCT	373	22.58	716
AB_PRBO_20	NA	NA	0.25	1	0.9	0.5	0	2 5 5 4	TTTCCATTCTTTTGGACACAACCTTAAGCAACTGG ATCTGATCTCATTGTAACCTGCTTTGAGCAGGAGG CT[A/G]GGAGGGAATAACCTGAGGTCCTTTCAAC TGAAATAGTGATGCTGCGATATCTTAAGCTGGGA GACAAAGCTC	254	30.72	794
AB_PRBO_21	NA	NA	0.5	0.25	0.1	0.75	0	2 4 5 4	GGAGCTGTAATGCCACACCAATGTTCTCTCAAC ACGGGTTTTAGGGGAGGAGGCAGCAGAGGGGA GAGCC[A/G]TGCTAGTCCCTTGTGGATCTGAT TTGATCTTCCACTAGTCTGGACTTCTCCCA	365	29.14	610

AB_PRBO_23	8	18544125	0	0	0	0.4	0	1 5 5 5	ACAGTCTGTTAAACTGCTCAATATTGGTATCAGTT TATTGACTGTGGATTGTCCCTCAATTACCAAGTGCCC ATT/CJGATGGCAGGAGCTAATGCACTGCAAAATCGC ATTGGAGTGCCTTTATTAGATTAACTTGATACAC GCTTATGTA	341	18.33	956
AB_PRBO_29	NA	NA	0.75	1	1	0.6	1	2 4 5 5	TTTGTAGATAAGGGAGGTTTGCAGGCTGTAGTTCTG AATGAAAAAGCTGTCCCTCCTTGGAAATGTA CTG CTG/CJTJTAATAAACGATTTCCTAGTGAAAAATAGG AATCAGTTTATGAAACATGATCATAATGTTGTCTCTC TTTGTGATG	300	12.17	249
AB_PRBO_30	NA	NA	0.75	1	1	0.6	1	2 5 5 5	AACAGCATATCCCAGATATCCATTTCTGGTCAAACT ACCACAATGAGAGAGGTTGGTAATGCTCTGGTCA GAG/GAJAGAGAGGAAAGTGAGGAGGACATGTGA GGGAAACAACATGGTGCCACCAAGTCACTGGA GAAGGAGGGGAGGG	303	48.00	2485
AB_PRBO_31	NA	NA	0.75	1	1	0.6	1	2 4 4 5	ACCCTTTGGATCTCTCATCCCCATGCCATTCTGTG CTTGGGAATCAGGCGCTGAGTGGCTGCAAGGCTGC TTG/T/CJCTGCACTGCTCTGCTTTTAGGGAGTGTG ACTAAAGTCTCCCATTTTGGCTCCCGGAGGAGAA GAGAAGCACAA	385	26.00	482
AB_PRBO_32	NA	NA	1	0.5	0.7	1	1	2 5 5 5	TAATACGGTGGAGGGCTGCTTGTCTATAATGAAGTA ATTTAACTGTGAGTGAAGGCTCTCATAAAATGTAA GTT/CJATTTGGGTCACTGCAATGTGAAGTTAGG TGTTGCTTCTTCCCCCTCCCTACTACGCTTATCAA ACTGAAAA	269	14.72	800
AB_PRBO_33	NA	NA	1	0.3	0.6	0.8	1	2 5 5 5	GAACATGTACACAACTAGCACTTGAACAAAGAAC ATCTGTATACGTGCGCCGCTCTGCAAGCACCAAA ACA/CJTJGTATGGACATGTACCTTGTATCAGCAG CAAGAGCAGGATTTCTAAGGGCTTTGGTTGGCT CCTCACATTC	245	22.46	893
AB_PRBO_34	NA	NA	0.5	0.5	0.8	1	0.7	2 5 5 5	TGAAGTGGCACAAACCTGAGCCCGGGGACATGCA GGCCCTGTCTGCCATTCTCTTCCAGCTGTGTTCTGT GCA/T/CJGGCGGAGAGGAAACAGGGGACGCTCAG GCTGTAAAGTCCCTGCTGCTGCTCCAGCTGCAC AGCACCGTAGCG	387	38.53	611
AB_SW_02	13	5182930	0	1	1	1	1	2 5 4 5	AACTTGATTGTTGATTGCTATAAAATTAACAGTTGT TCTGTCTAATCATTGGTGACACAGGGACAGCTG TT/CJGJTTCCTCCTCATCTTAATCACTTTACCATTTT ATGGTGGTTCTTTCATGCTTTCCTGGGTTCTCTTTTC TGTAAC	378	17.09	184
AB_SW_04	24	573576	0.25	1	0.875	1	1	2 5 4 5	AATCCCCTCTGTATGGCTTTTTTATTAAGATAAAA AGCTGGAGTTCACAGGAGTTAGCATTAAAGTACAG TC/CJAJAGCAATCCGAGGTACTGCTGGCTGGG GACTCTCTCTGTTTATTCAAATACCCCTTATCATCC TGTTGAAAG	489	9.98	486
AB_SW_05	NA	NA	0.25	1	0.8	0.9	0.2	2 4 5 5	AAAAAAAAAACACTCATGTACTGCTTAAGTGACA[ A/CJT]TCCCCCTGCATCACATCACATAAATCAAA AAATAACAAAAATGCGAGCTATTGAGCTTCCAAAAAT TTGCCA	198	22.18	487
AB_SW_07	1	52977777	0.5	1	1	1	1	2 5 5 5	AATGCAGTTTAGAGTGGCAGTGGGAAGGGAAGTG CTAGAGTTTGTATCCATATTTCCAGCACATGTCCATT ATAC/AJGAGGATGGAAGTTCTGGTCTGGTCACCTC TATCTCCCTCAGTGACAAATATGATGTGCTATCATGA GGATGAGTCAG	296	10.03	659
AB_SW_08	1	74621794	0.5	1	1	1	1	1 5 4 5	TATCAAGCAGCTTTCAGTGGCTTGTAAAGATGAA TTCCAGTCCATCATAATTAACCTAAAAGTCAGCTGC CT/TJ/CJCTGTGTCTAGTTTCTCTGTGTTCTTCTCCC CTTTAGTTTGTCTTACTTTGATGTTCAAGTTTGT TCCCT	397	20.15	244
AB_SW_11	3	31465368	0.5	1	1	1	1	2 5 4 5	GATTTTACTTGTCTGCCAGCTTACCCTGCTGGA GAGGCAGACTGTTCACTGTTGGCATGCATTTCTC CA/CJGJATGCAGCTGTTTCCAGCTCTCCCTGTTTCA CCTGGGTTTTTGTCAATCATCTCTTGACAACCTTG AAGTGAA	269	10.23	362
AK_PRBO_01	1	19055546	0	0	0	1	0	1 4 5 4	CCCCACTGTTACTTCAGAGTGTGATCTTCCCTCTTA CTTCTGGTAATTTATTAGGTTGTAACAAAGCTGA CG/GJTJGATTATCACTGGTTTTCAAAATGCTCTG AACTGAGAAAGGTCAACACTCTCACAGCTGTTGTTG CAGGTTGT	340	26.70	685
AK_PRBO_02	NA	NA	0.5	0.3	0	1	0	2 5 4 5	ATTTCTAAGGCGTAAGTGTGTTTTCTGCCAAGGAGGG ATGAGGGATGTGAAATGAGACAAATAATGGTAAA GGAA/AJGJGCGTAGCACCCAGTTCAAGTGGCCAAA TAGTCATGTTGGTGGGAGAGCCAGACACTTCTTAGA GGTAAGGAAAGG	367	24.61	581
AK_PRBO_03	NA	NA	0	0.625	0.125	1	0	1 4 4 4	CTCACTGGAGGAACACATAGTAATTTATACCCAGC TATTGAAGAAGATGAGGCCAAGCCCTGAGTGACAG ACAC/AJTJTGATGAACAAACATGAATGAACAA AATTGTACTAGAAAAACAGTAAACAGAAATTAATCA TTGAGGGCCCT	379	15.43	785
AK_PRBO_04	7	22925324	0	0.5	0.1	0.9	0	2 5 5 5	GGTTTCCCTTTCCCAAGGGGAGGTCAAGCATGGC TCTATGGCTGGGTCCAGGGGATTGCCATCATGGT TGGGG/T/CJACGATGACCACAGCATGTCCACAGC TCAGCTGCACTGGTCCCCTGCGAGCCAGGAGAGT GCATGGAGAGCA	390	38.71	1505
AK_PRBO_05	1	55121471	1	0.5	0.25	1	1	1 4 4 5	TAGGGGTAAGTGTGTAGGGACTGTTGCTGTCTG GAAGAAAAAGAGAAAAAACCACTTATTGGTA CATTTA/JTJACTCTTACAGCAGAAAGGAGGTTTT CTGATAGACTGTACTGCCAAACATACCTCATGG TCCTGAAGCCA	355	26.20	684
AK_PRBO_06	1	87374294	0.5	0.9	0.3	1	1	2 5 5 5	TTGTTACTGCTGGAATCATTTAAGGACTGATTA GCTGGCTTTCTCATCTAGGCTGATTTCCATAGGAAA CA/JG/CJGCTGTGTGGCCACTCTGCTGTCCTTTA GATGTGCACCTAATCACAGTAGTTTGATGCAAG TTCATTCA	337	27.61	1005

AK_PRBO_07	NA	NA	1	1	1	0.3	0.7	1 5 5 5	GTACAGAAATTTGTTTAAATCCAGCTTTACTGAAT GTGCTTCTGAAAGCACAAGGTACTGATCACACTTC TG[C/T]CTGATTTTGGGTTACAGTGACAGTGCAA AATGTCAGAAATATGAGTAAGTTAAAAAGCAGTGCT GAGTTGTA	277	10.95	369
AK_PRBO_08	1A	50103968	0.5	0.8	0.25	0.9	1	2 5 4 5	CCTACCCAGGTGTTTCTGTTTCATGACTAGCCCA CAAAAAAATAATCAATCTTGATTGAATTTAACTC CC[G/A]TGTATATTAAAGCTCATAGCTGGAACATC TCTGTTTTTGTCAGTGGTTCACTTCTCCCTTCCCTCT ACTGTTG	233	22.71	714
AK_PRBO_10	1A	48784106	0.75	0.75	0.375	1	0	2 4 4 5	GAATGGCATCGTTTGGGAATTGCCTGCTGGATAAG GAATGAACCTAACGAGAGCTTGGATAAAGCAGCTCA TTTT[C/T]AAAGTGTCTCCCTGCTGCTCACTCCATCG GGATCTCTTGAGAGACCTACACCACAGCTGGAAAT TGCATGGGAT	315	21.46	759
AK_PRBO_11	2	27946810	1	0.6	0.4	1	0.9	2 5 5 5	CATGCACCTTTTCAACCTGTAACTCTAACATAAAA AAAAAACAAGTGTGTACATTAGAAAAAAGGCCA AAT[G/A]CCTAGCACAGCTGAATGTTTTACTACACA CAATTCTCCCTTAAGAATAAATGCAAGGTATTTGAA GGAGATTCTA	409	34.58	1334
AK_PRBO_12	NA	NA	0.5	0	0	0.6	1	2 4 5 5	CCTTAGAGCACAAGAATTGCAGCCTTTGCGAGATG AAAGCAACCTTTAGAGGATAGAAAGATTTCCTCAA AAA[C/T]ATGAGGCTTCACTTTTACAGTCTGCATT GCAACATGACATAAAATCCATGCGACAGTACTCC TGGTTTTG	296	29.49	825
AK_PRBO_14	NA	NA	0	0	0.2	0.75	0	2 4 5 4	ACCCTTCCAATCAGAGACTTATGAGATGTTGCACAT CCTCTGCCAGAGCTGTTCCACCTTCTGTGGAATCC CC[T/A]CCTGAGCTCCAAGATGTGTGGGCTGCTCC CCACACCTAGCAAGGGCAGTGGCAAGTGGGCAAC TGACCCAGCC	254	43.19	737
AK_PRBO_15	1	91999876	0	0	0	0.5	0	2 5 5 5	TAAGATGATCGTGTGTCCTCTAGAAAAATCAGCC TCACAGTGGAAACGAGGCCCTGACAGAAAGGCA GTGAT[C/G]CTGGGGAAACAGCAAGGGGATAAAC AGCTCCGGGCTGCCCTTACTCACGCAGGATGCAG GTGCTCAAGTGCGA	427	30.21	1717
AK_PRBO_16	2	17653584	1	1	1	0.5	1	2 4 4 5	AAATGATAAGACAACAATAAAACAGTTTCTAAA AAGAAACCCCAAGTGAATGCAAGTTAGATGCACATA CTA[T/C]CTTCAGAAATGTGAGCTCAAGCTCAGAG TTTATTGATTGTGGCTCAGCGCTGGTTCTGCTAGATT TGCACTCT	431	38.19	820
AK_PRBO_17	2	72818899	1	1	1	0.5	1	2 5 4 5	CTGAATCTAACATCTCTGCCTCTTCACTGCTGTTT CATGGCTCTGTGACTCCTCTCTCTGCTTGTGACTCG C[C/A]TCTCAGAGCATCTTTGTTGCTCCCTCTCCCT AGCAGAGCAGCCC	174	35.10	729
AK_PRBO_19	24	5589755	0.25	0.4	0	0.5	0.2	2 5 5 5	CCCCGTCTGTTTGAAACCCAAGGAAACCACTCT CAGAGGAATAAATAATATATCAACACAGCCGACA GAAA[C/T]GCTCACAACTTAAGCTGGCCTGACACA AAGGAATAGATAAATAATGGAGAGGGAAGGGGGA AGCCAACACTGCA	221	24.19	886
AK_PRBO_20	1A	48656370	1	0.5	0.5	1	1	2 5 5 5	TTTCCTTCTGCTATCAACACCTCTCTTCCACCC AAACCCACAGCACTGGCAATCATCTGACAGCCCA GA[G/T]JACAACTGGAAGGTGTGTTTGGATGACATCT GTGCTAGGTGTGTCACCTGCAAGTAGGGAAGCAAGG GGCTTGCTG	364	31.31	1857
AK_PRBO_21	NA	NA	0.5	1	1	0.5	0.125	2 5 5 4	TAATTGCAATTTTGTCTAATCTGTACTGGCTAGAAA TGGAAACTCCAATTAATAATGGAATAATATTCT GC[A/G]TCTAGTAGTCTAGAGAATAAAGAGATTCA AATATCCCTGCTGTACAGCAATTATTTAAACATTTTG CATATTCA	259	22.96	504
AK_PRBO_22	NA	NA	0.5	1	0.5	1	1	2 5 5 5	GTGTCAGCTCCCGGAGCACAGGAATGGAGGGTCC GGGCTCAGGAGTGGGTGTCCCTTCCAGCATTTCC TGAC[T/G]CAGAGAGCCCAAAACAGCCCTGTGCTCC TCAGCCCCATGGCACTCTTGGTCTGTGGCACCATC GCTACCCCTTG	316	17.81	1072
AK_PRBO_23	1A	54877748	1	0.9	1	0.6	1	1 5 5 5	TCCCCAAGAATGAATACCTATATAATCTCTATCA GCCAGGAAAAATCTCAAGGCAGACTAGGTGCTTCA CT[C/T]TGTATGAAGAGAGGGCTCTCTATGGCTGA CAAGGGACAGTAAGAACTACAGAACTTGGAAAA GGCCACAGAAT	279	34.84	521
AK_PRBO_25	NA	NA	0.25	0.5	0.4	1	0.5	2 5 5 4	AAAAATAGATATTTTGTAGCTTCTCTGGGTGTTT TTTCTGTCTGCCATATGTGTGGTGAGCTCTCT C[A/T]GTACGTGGGTGTTTCACTAGGCTGTGAGTCA CTGCTGCAGGCACAGCAGCTGAGGGGCTCAGTGTG GGGCTCAGC	221	33.21	1281
AK_PRBO_26	NA	NA	1	0.7	0.4	1	1	2 5 5 5	AGTAACTATCTAAAAATATTGATTGCACTGTCTGT GCTTCTGCTCTCTGCTCTGACCCGTGGCTCCTCTT GT[C/G]TAAACACACATTCTTTGGTTGGTGAGAGAC ATAATGATGGTCTGGTTCCATAAGCTGAATACAGT TTGTTTAA	241	10.08	835
AK_PRBO_27	NA	NA	0.75	0.75	0.4	1	0	2 4 5 5	AGGCTCCCAACAGACAGCTCTGTGCTTCCCTT CCTTCACAACTCAAGGATGCGACATTCAATGAGT GC[A/G]TCTGAGCTCAGAGCCCTCATCCTCACCC GGTGTCTCTGCTGTTTATTCAAGCTTAATGCCAA GGCAAATAA	448	27.98	1162
AK_PRBO_28	NA	NA	0.5	0.5	0.9	0.375	1	1 5 4 5	TTAGTGTAGTACTGTGTGGCATACAGCCCTCAC TGGCTTGCCTTATGTAATCTAGGCACATATGTTTC AC[A/G]TTCAGTCTTTCAATTTCAATGATGATTT TACATTTTTCATGTTACAGGCAGTGATTGATTGTG GATGCC	462	13.63	603
AK_PRBO_29	NA	NA	1	0.625	0.5	1	1	2 4 4 5	ATTCAATTTCTGCTGGCTATTGATCACCTTTGATGT TAATGTCATCTTCACTTTTGTCTTAAACATCTT T[C/T]CCCAAGCCAGGTGTCTCAACTGCATAGAAG TGTAAATGTTCAATTATGTCGGTTAATAGTTATGTTT TATCT	351	15.08	356



AK_PRBO_32	NA	NA	1	0.9	0.5	1	1	2 5 5 5	TTGTTGTTTGTTTTTTTTCCACAGACTCATGTAG TTGGGTTTTGGCAAGATCACACCATGCCCACTGA A(C/T)GTGTTTTGTCTTGAATCAGGTACTCAAGCATG CATGGAAAGCGCTATTTCGCCAGTGATCACTTGC ACAGTAG	253	23.73	513
AK_PRBO_33	NA	NA	0.5	0.9	0.25	0.7	1	1 5 4 5	ACGAGGATTAAGAGAGGACTACATCAACAGTGC TCTACAGATGAACCAAGTCTAGATGAACCAAGAGA ACACA[A/C]GAAATGAAGTGCAGGGAAGAGAAGG ACAAATTGGGAAGATCTCTATGAGCTGTGTGTGCA GCAGTGCA	421	38.79	804
East_West_01	Z	66755642	1	1	1	1	0	2 5 5 5	TATTTAGTAAGGTATGGCTACACATTTATACTAATTA TTATTACTTGAATAGATTTCATACTTTGGGTAAG GT[A/G]CCTCTCACCAGGCTGTGGTATAATTGTACT AGAATACTGTTTTCTTCCAAACAAATGCAGCAAA TTAGAAAA	263	27.01	844
East_West_03	Z	23626857	1	1	1	1	0	2 4 5 4	AGTGGCTGCTTGCACAGCAGTGAAGTAACACAT GTGTGGGATTTTGACAAATGTCTTGAAGAGCAGCTG AGCT[G/T]CTCAGTTGTGTGGGTGCTGTAAAGG GTACTGAATGATCCTAGAGAGGGCCTAATGCCAGT ACAAAGGAAGT	282	19.42	499
East_West_05	5	14184645	1	1	1	1	0	2 5 5 5	CACCTGATTATTTCTAACACAGGTCACCATTTTTAT GAACCTTACTGACCAAAATAATTTCAAGTTCACACT A[A/T]JAGGGTTTTCCACCTACACACATTAGATCA GGCTTGTGCAAGTCCATCTTTTCACTCTTCCACT CCCACT	353	8.13	443
East_West_10	18	9024958	1	1	1	1	0	2 5 5 5	TTCTCCCTGGGCTTTGGAACATCAAAACAGCAGAAT AATCCATTCCATGGTTGGACTCTGCTCCCTCACAG AT[C/A]CAGGAGGAGTTTTGGCTGCTTGACCCCTCC TGCTGGCTGCTACTGACCCCTCACACTGACCTGGCT GTGCAGGAT	350	45.73	1272
East_West_12	1A	51827765	1	1	1	1	0	2 5 5 4	AATCCTCTGTATGTTCAATTTAAAGCCTGAAAGACA AGATAGCCCATATAACAGCAGCAGCAATTTCCATA AAG[T/C]GCCAGTTTACTGAGAGCCCACTTCATTTA ACAAAGTGTGACCAATACTGG	201	25.44	702
East_West_15	6	15555868	1	1	1	1	0	2 5 5 5	AAATAACCTTGCAAAATGAAGCATTGCATCCCTGT AATACACAAAACATTCTAGAGTAACACTCGGGACA AGG[T/A]TCTTCCAGAGAGTCCCAACCAAGCA AAAACAAAAGAACCATGAATAAAAAAATGAGA GACCAAAACAC	386	19.21	954
East_West_16	Z	31672467	1	1	1	1	0	2 5 5 5	ATGTTTTATGCATTTTTTTTTCACACTGGACAACCA GATCTTCTGCTGCAGCGGAATCAATGTTTCAGACGG AGAT[T/C]AACACAGCTGAGACAAAGTTACTGAGAAG CTCTGGGAATGAGAGGCAAGGACTGACCAAGACCA TGTCCTTGTC	330	35.54	1582
East_West_17	3	50903092	1	1	1	1	0	2 4 5 5	GAAAGATGCCGGGAGAGGGCCAGCGGGATGGCA TCTCAGGGAGGGAGAAACCTGTTCTGACATAAATT ACTGA[T/C]TCTCTGTGCTCTGCAAGGAGTCAATTA GGCACCAAGCAATGGTTAACAGGATGGGTGAAGGT AGCCAGAACAGGC	370	19.04	742
East_West_18	5	6669499	1	1	1	1	0	2 4 5 5	CCACAGGATGGAGGGCTGGAATGGGATGGGGACA CCCACTGCAACCAAGGGGACAGGGGACAGCAATC CCGCTC[T/C]GACACCTGGATTTCCAGACCACTTTG TCCTTTCGCGCTCGGGATCCTGGCCGGGATACTCC ACCTGCCACGTG	421	31.29	637
SW_AK_02	NA	NA	0	0.75	1	1	0	2 4 4 5	CAGGTACAAGGCTGAGATGAGATCTTAGCGATAA CAAAGTTTATAGGAGACATTGCATGCTTGAAGTGTA GCA[A/G]AJAGGTATTGCTGGTTTTCACAGCTGTG AAACAAGATGTAATAATCTGATAAAGTACAAAA GCAAGAAACCA	346	15.29	666
SW_AK_03	1	93977276	0.25	0.625	1	1	1	2 4 5 5	GGAGATAACACACACCTCAAAACTGCACAACCTCCC CATCTCTGTGGCACAGGACAGATGAAGCAGCCCTG AGG[C/A]ACATCTCTCTTCCCACACTTGCTCTCTG ACATCTCTTCCACCTAACACTCACTTCAGCGAATGCT AGGATGAG	437	17.83	980
SW_AK_04	1A	39550183	0.25	0.9	1	1	1	2 5 5 5	TAAAAATATAGTATCCCTGTGAGATTACACTTTCTTG AGTGATATGCTGAAAAAACCCAAAAACCTAAAA AAC[C/T]TCTCTCTTTTATTATTATTCATTTGATTT CAGCAAAAGTCATGCTGAGCAAGATAAAAAACAAAC AAATGAAAC	341	12.67	622
SW_AK_05	NA	NA	0	0.75	0.75	0.7	1	2 4 4 5	ACACACCCTGTTTTATCAGTAAGAAAAATATCTGA AGTGGCAAGGCTGATTGAGCTCTCATACAGATACA ATC[C/T]JAAAGCAATTCCTCCACAGAGAATGAAAG TCCTGAAAAATTCAATCTCTCCACAGGGTTTATACAT TTTGGGTTT	266	28.75	733
SW_AK_06	5	49236409	0.25	0.8	0.9	0.8	0.8	2 5 5 5	TCCAGGGTAATGAGATTGAGAAATTAATACAAAC ATAACTCCATCTGATCATCTTCAGCTCAGCTCTG GC[A/T]JGGGTAACTATTAAAGACATTTTCCACTG AAGGAAATATATGCTGTGCCACCTTTTACACCTC CTGGGCTAA	359	17.75	727
SW_AK_07	NA	NA	0.25	1	0.9	0.7	1	2 5 5 5	ACTCAGGCGTGTGCAAGCCTTTGATATGGGAAG GAAATGCTTTTAAAAAGAGCTGCTTTCTTTTGG GG[C/T]AJCTGGACCTCAGTGCACTATCAAGGAAG CTTATGATATCTTTCAAATCAAATAGGTGTTACTCTG GAATGAGAC	271	32.87	753
SW_AK_08	NA	NA	0	0.9	0.625	1	0.6	2 5 4 5	AGCACCTCACAATGTCAGGGACAGCATATGGGGT AGGCCAGACAATCTACATCTCTTTTGTCTATTGCG TG[C/T]GJGTGCAAGATCTGCATATTGTAGTGCTG AGAGCAAGAGGATGATCCTATGCATCTTTACTA GCATCTTGAT	200	44.64	839
SW_PRBO_1	NA	NA	1	0.75	0.5	0.375	0.875	2 4 5 4	TGGAGACACAGAGCTTTGCCCTTCCCTCTGTGAAAA TCAGTTCAAAATGAGTAGAGAGGAAGAGACAGGA GGTA[A/T]JGGAGAGTTTATGCAACACTAGACATCA GGAAAAAGAAAAAGGAAAAAACAGGCTGGAG AAAAACAAGGAAAGT	360	13.71	765

SW_PRBO_2	NA	NA	0	1	0.4	0.6	0.4	2 4 5 5 5	AACGTTAATGAATTTCTTTTGAGGAGAAGGACAGCA TTATTTTCAAGAGAATGATTCAGAACAGTTCTGCC AC[A/T]GTGGCTCAGCCTGACTAGCATTGTTTTT CTGAGAACTCCACCCAGGGCTTACACATGTGAGAAT GTGTGTAA	338	25.84	1008
SW_PRBO_3	NA	NA	0	0.5	0.25	0.6	0	2 4 4 5 5	CAACCGAGCAGCCATGCCCTGCATGTCACCCACGG TGACAGCCGCACCTGCATGCCCTCTGTGGCAGCAC AGG[G/A]CTGAGCTCTGTGGAGAAGGGAGCCTGCA GTGCAGGGGATGCTGAGATGGGTGCAGATCTGCAT TTGCAAGCTGCC	407	31.49	689
SW_PRBO_4	NA	NA	1	0.7	1	0.4	0.1	2 5 5 5 5	TTACAGCCTGTTACATATTTAATGGTGTGTGAC ATTTCCCATTTGTGAGCTGATTACCTTAATTGCCAGT A[C/T]TGCTCCTGTTCTCTGATGGAATGCCACTCACG TGAGTGAGAGCTGCTCATAAACATGAGCTGTTCATA AACATGG	185	42.12	1357

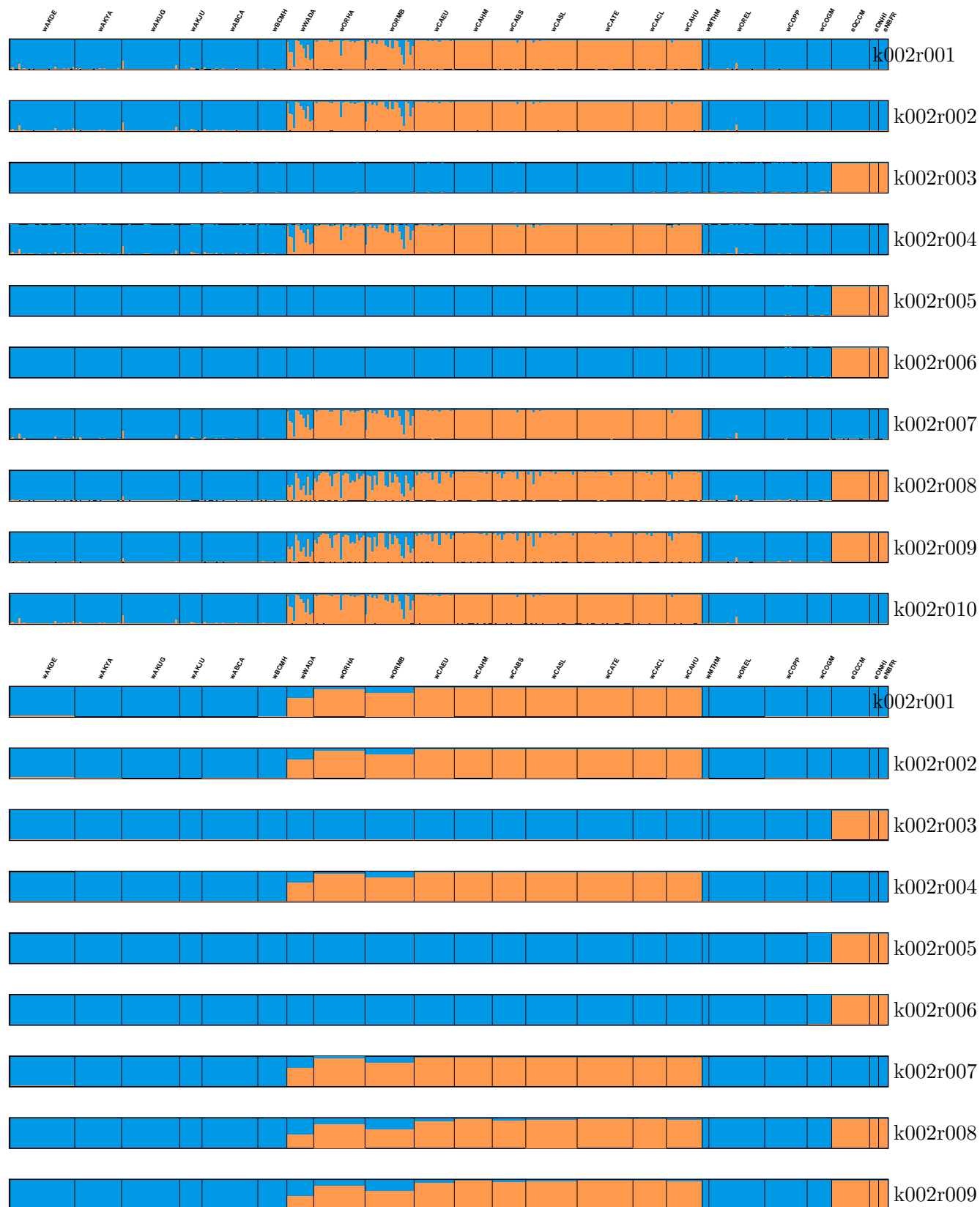
**SI Table 3.** Fst calculated according to Weir and Cockerham. Values with \* are significant at the p<0.05 level. Population names associated with each letter are listed in Table 1 and Figure 1b.

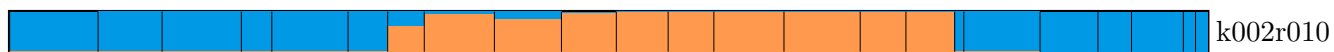
[illegible]

**SI\_Table 4.** Assignment of wintering & migrant birds to breeding regions using GSI\_Sim. Population names are listed in Table 1 and Fig. 1b.

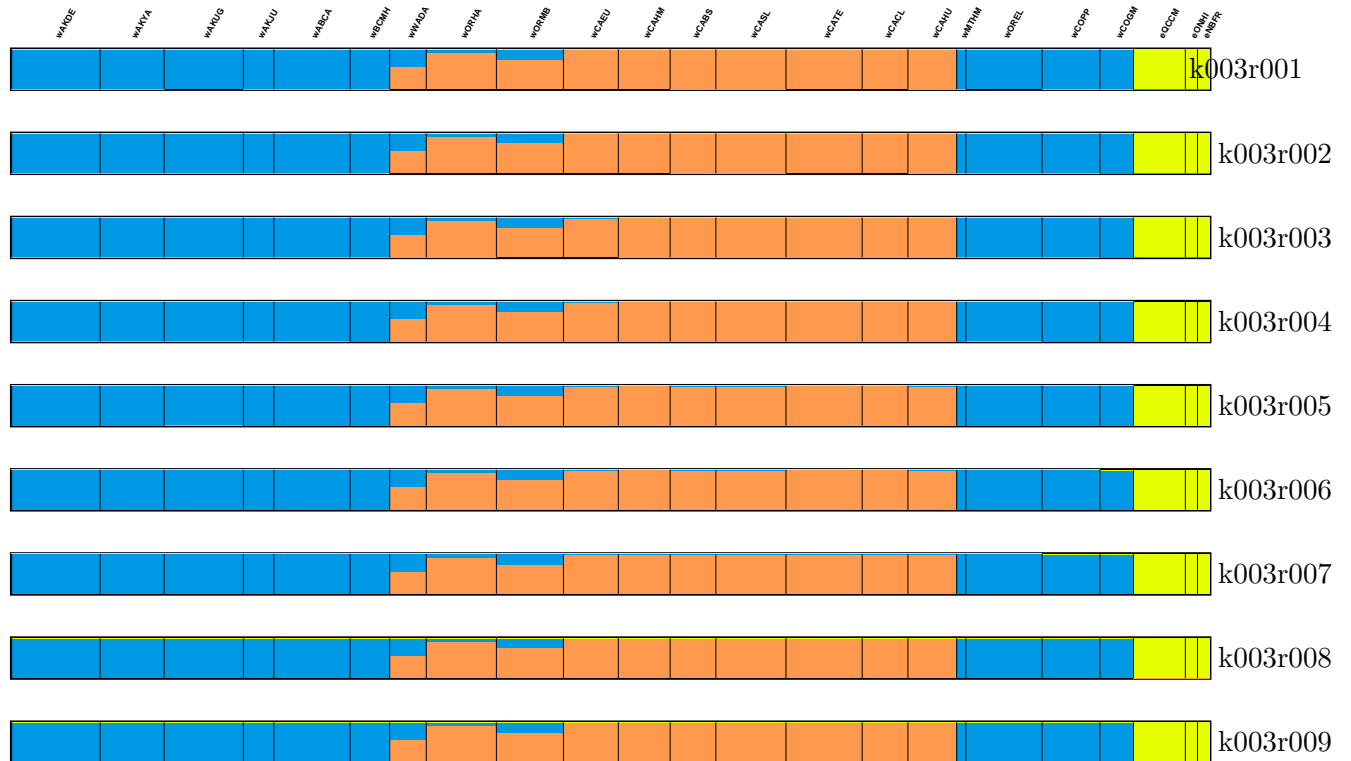
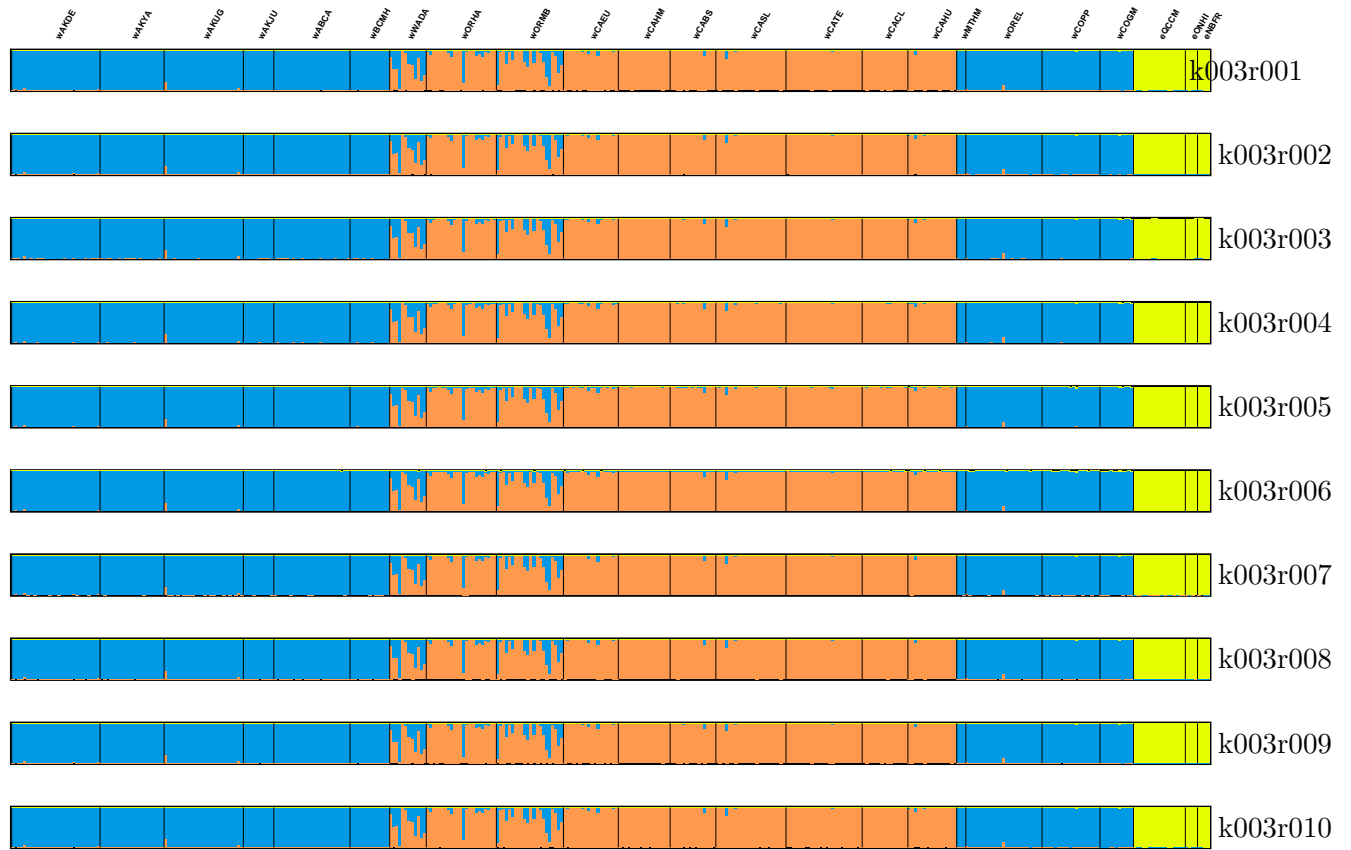
<b>Population (Fig. 1b)</b>	<b>Population</b>	<b>Alaska to Alberta</b>	<b>Pacific Northwest</b>	<b>Coastal California</b>	<b>Sierra</b>	<b>Rocky Mountain</b>	<b>Eastern</b>
<b>Wintering</b>							
<b>h</b>	<b>Baja</b>	0	1	7	0	0	0
<b>i</b>	<b>Sinaloa</b>	0	2	5	1	0	0
<b>j</b>	<b>Jalisco</b>	28	0	0	0	0	0
<b>k</b>	<b>San Angel</b>	9	0	0	0	0	0
<b>l</b>	<b>El Cielo Biosphere</b>	15	0	0	0	0	0
<b>m</b>	<b>Veracruz</b>	20	0	0	0	0	0
<b>n</b>	<b>Oaxaca</b>	14	0	0	0	0	0
<b>o</b>	<b>Tuxtla</b>	3	0	0	0	0	6
<b>p</b>	<b>Belize</b>	0	0	0	0	0	1
<b>q</b>	<b>San Salvador</b>	50	0	0	0	2	0
<b>r</b>	<b>Tegucigalpa</b>	23	0	0	0	3	0
<b>s</b>	<b>Honduras</b>	11	0	0	0	1	0
<b>t</b>	<b>Monteverde</b>	4	0	0	0	5	0
<b>u</b>	<b>Puntarenas</b>	14	0	0	0	3	5
<b>Migratory Stopover</b>							
<b>d</b>	<b>Albuquerque, NM</b>	11	0	0	0	1	0
<b>g</b>	<b>Braddock Bay, NY</b>	0	0	0	0	0	19
<b>c</b>	<b>Buenos Aires NWR, AZ</b>	59	12	0	0	0	0
<b>b</b>	<b>Cibola, AZ</b>	400	135	63	6	0	0
<b>f</b>	<b>Fairview, TX</b>	1	0	0	0	0	42
<b>a</b>	<b>O'Neill Forbay, CA</b>	41	27	5	2	0	0
<b>c</b>	<b>San Pedro, AZ</b>	51	1	0	0	0	0
<b>e</b>	<b>Sierra del Carmen, MX</b>	7	0	0	0	0	0

**SI Figure 1.** Results of the population genetic analysis for Wilson's warblers across the breeding range using STRUCTURE. The following figure depicts the output from all 10 runs at each K value (K= 1-9) and the data are plotted using the program Distruct.





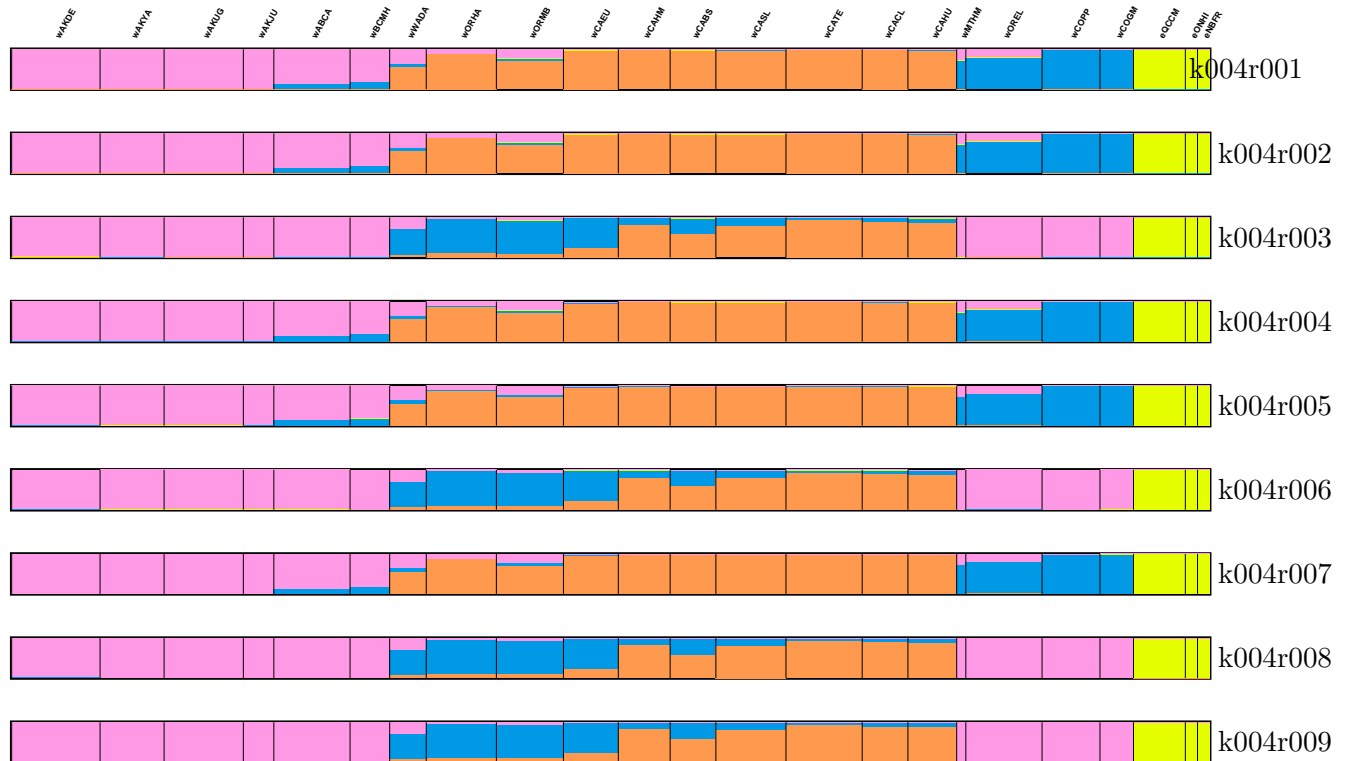
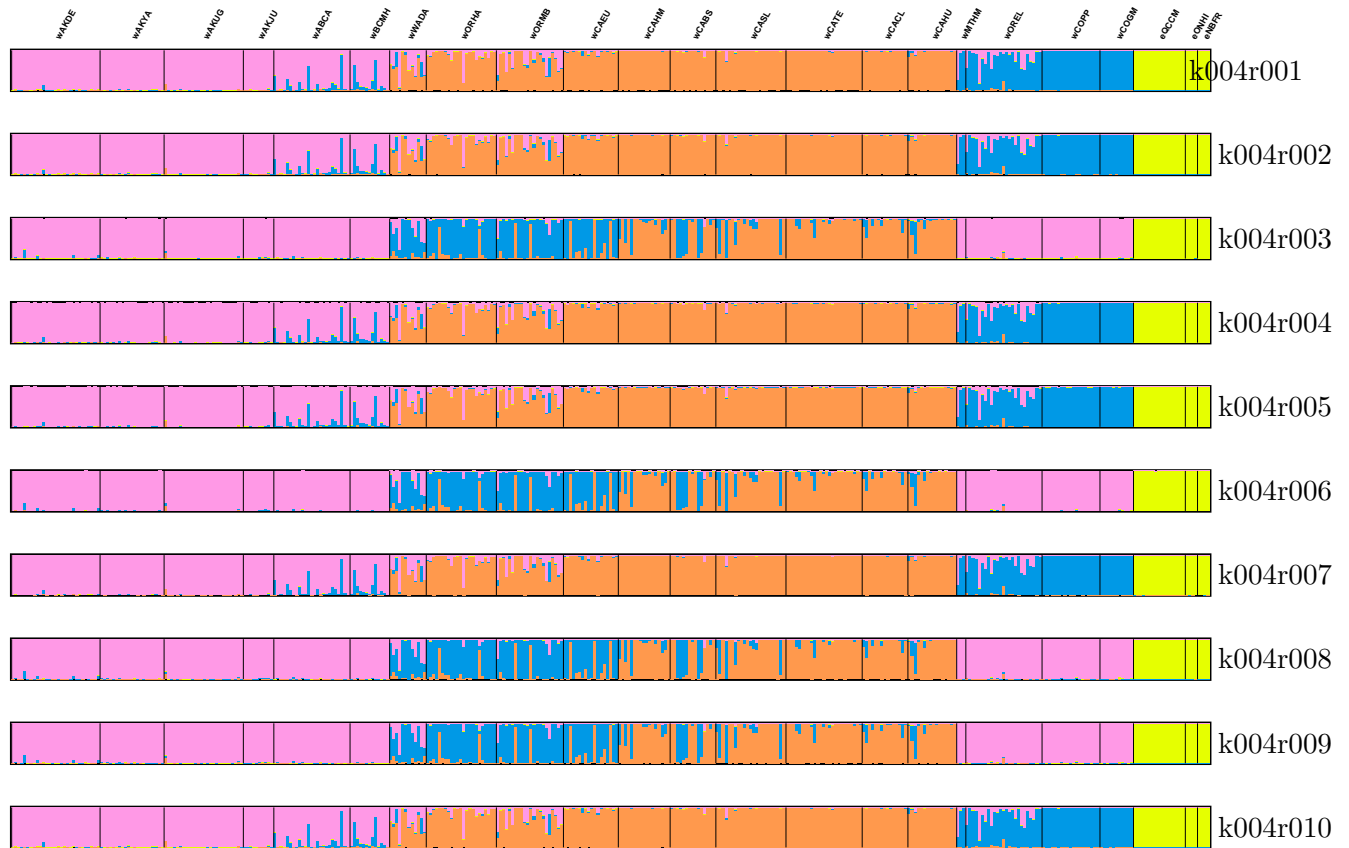
Distruct Plots at  $K = 2$ .





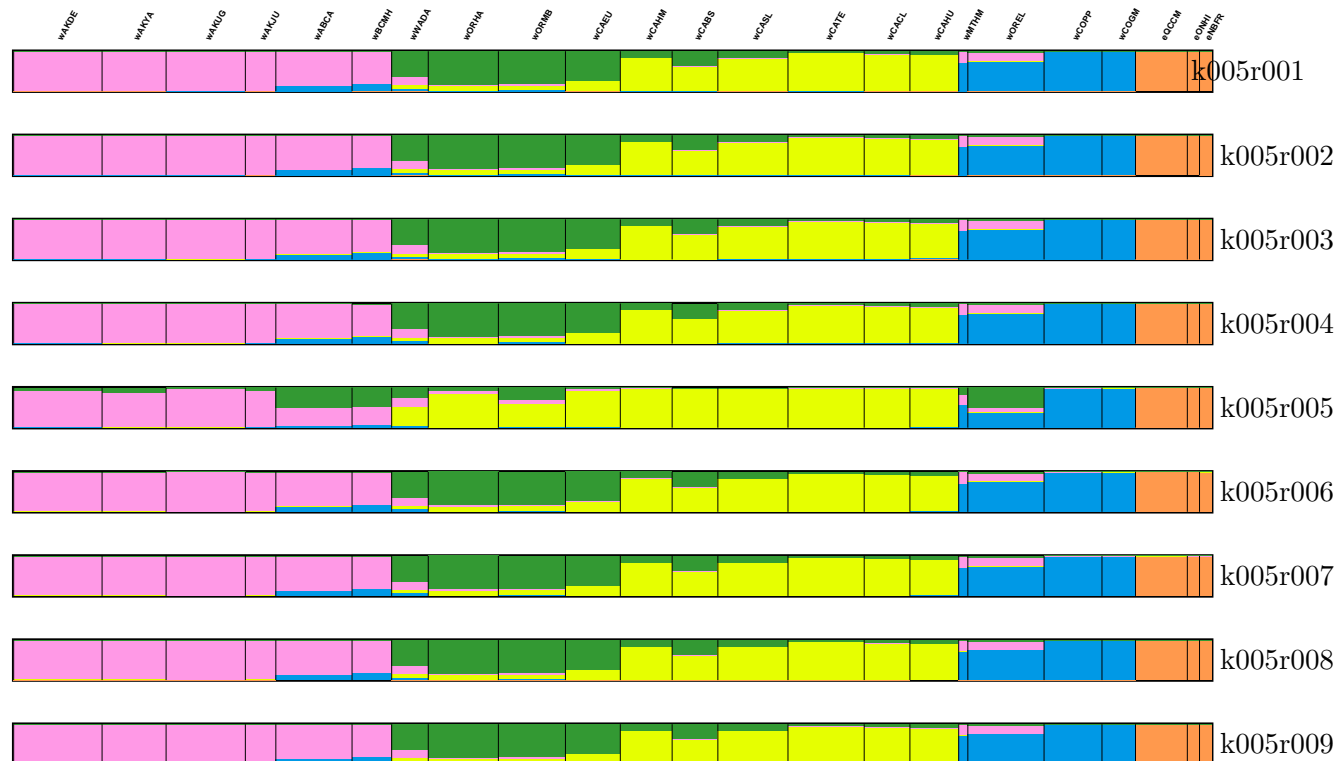
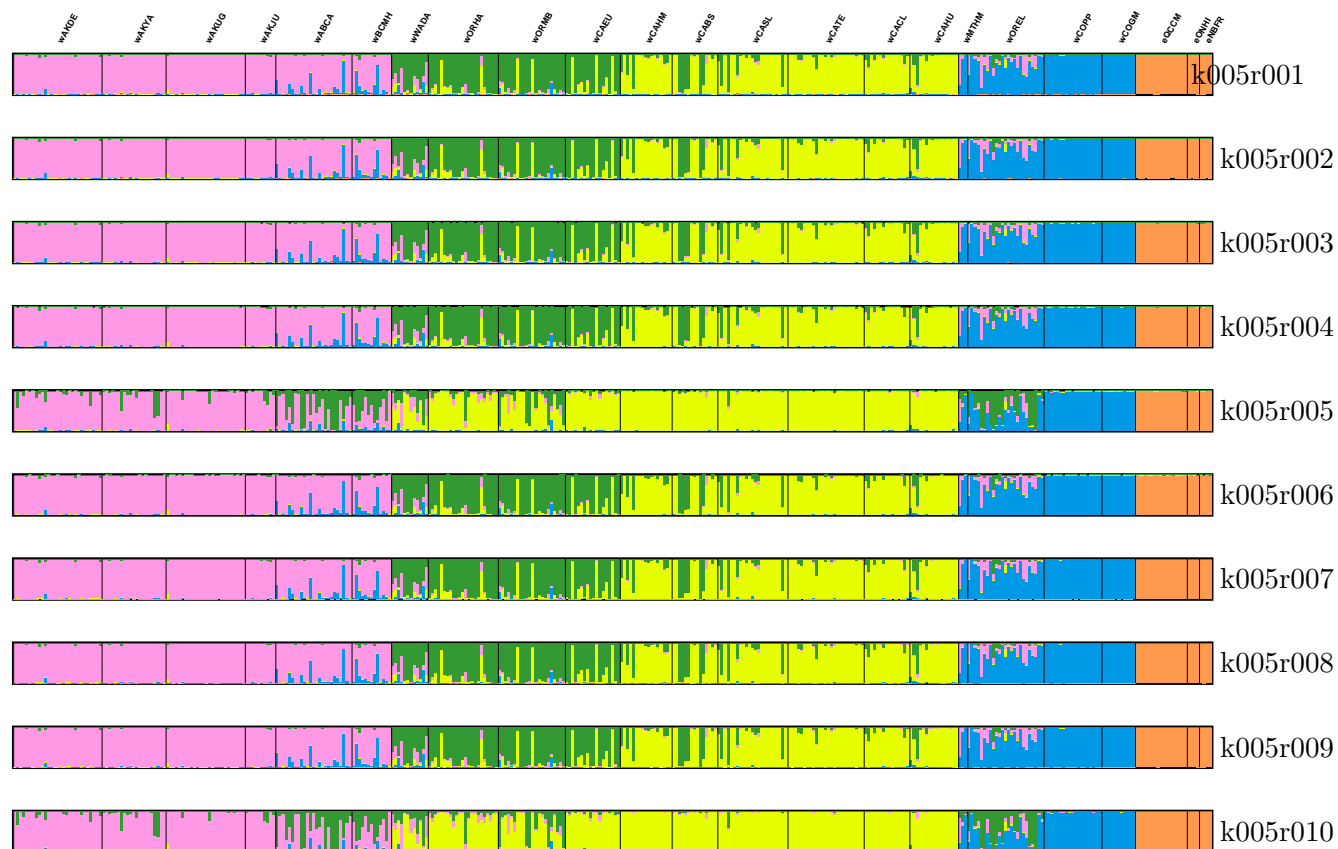


Distruct Plots at  $K = 3$ .



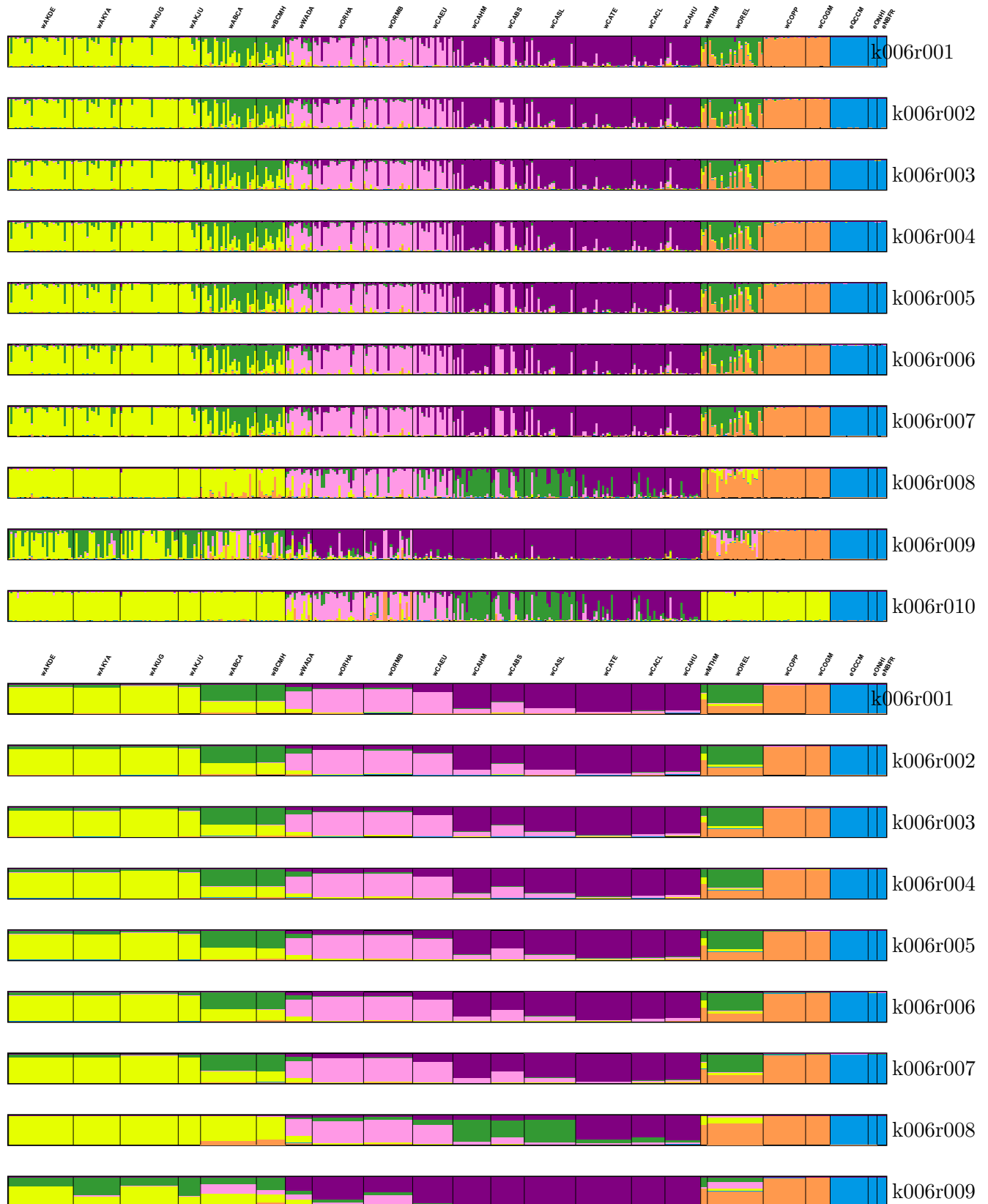


Distruct Plots at  $K = 4$ .





Distruct Plots at  $K = 5$ .





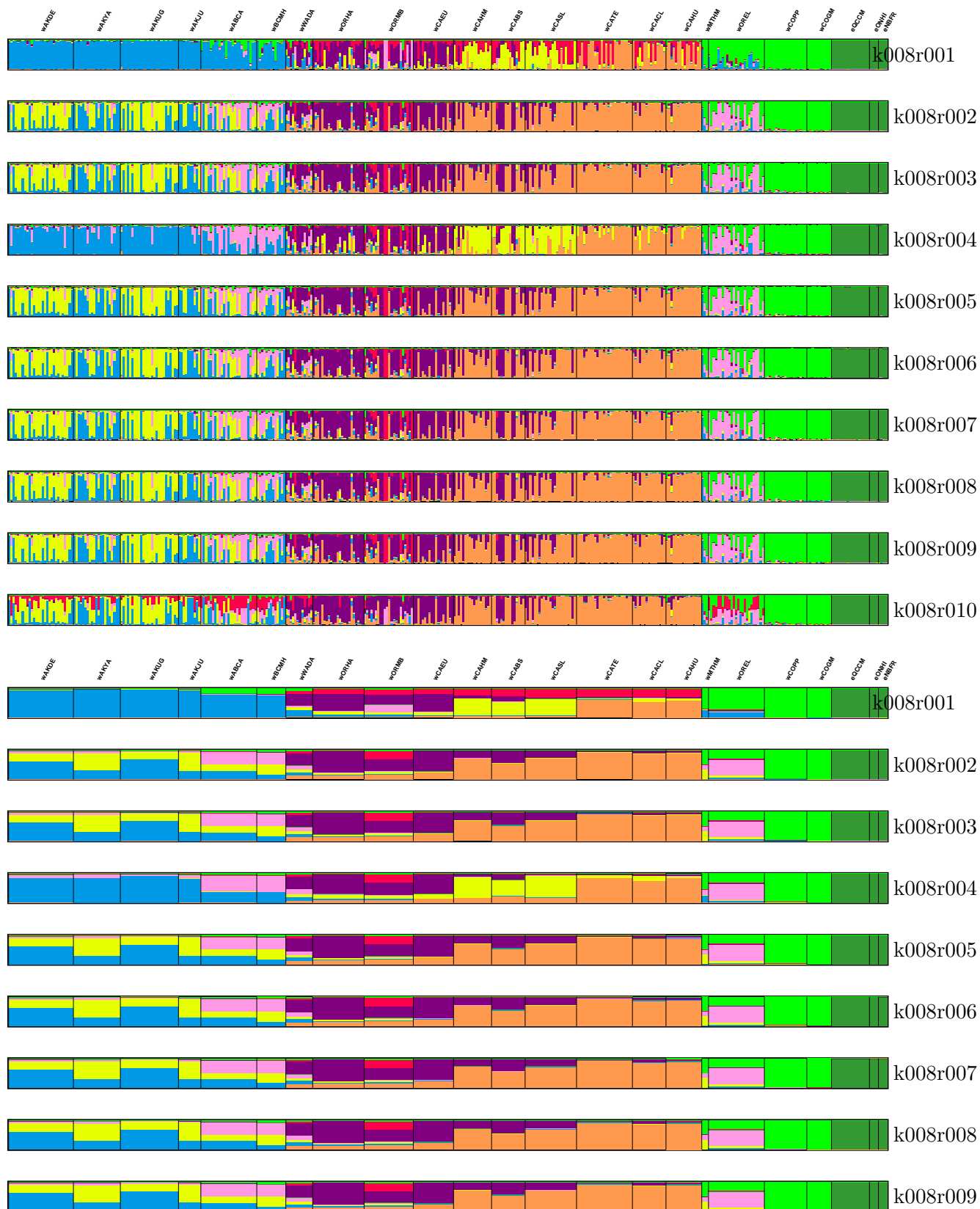
Distruct Plots at  $K = 6$ .





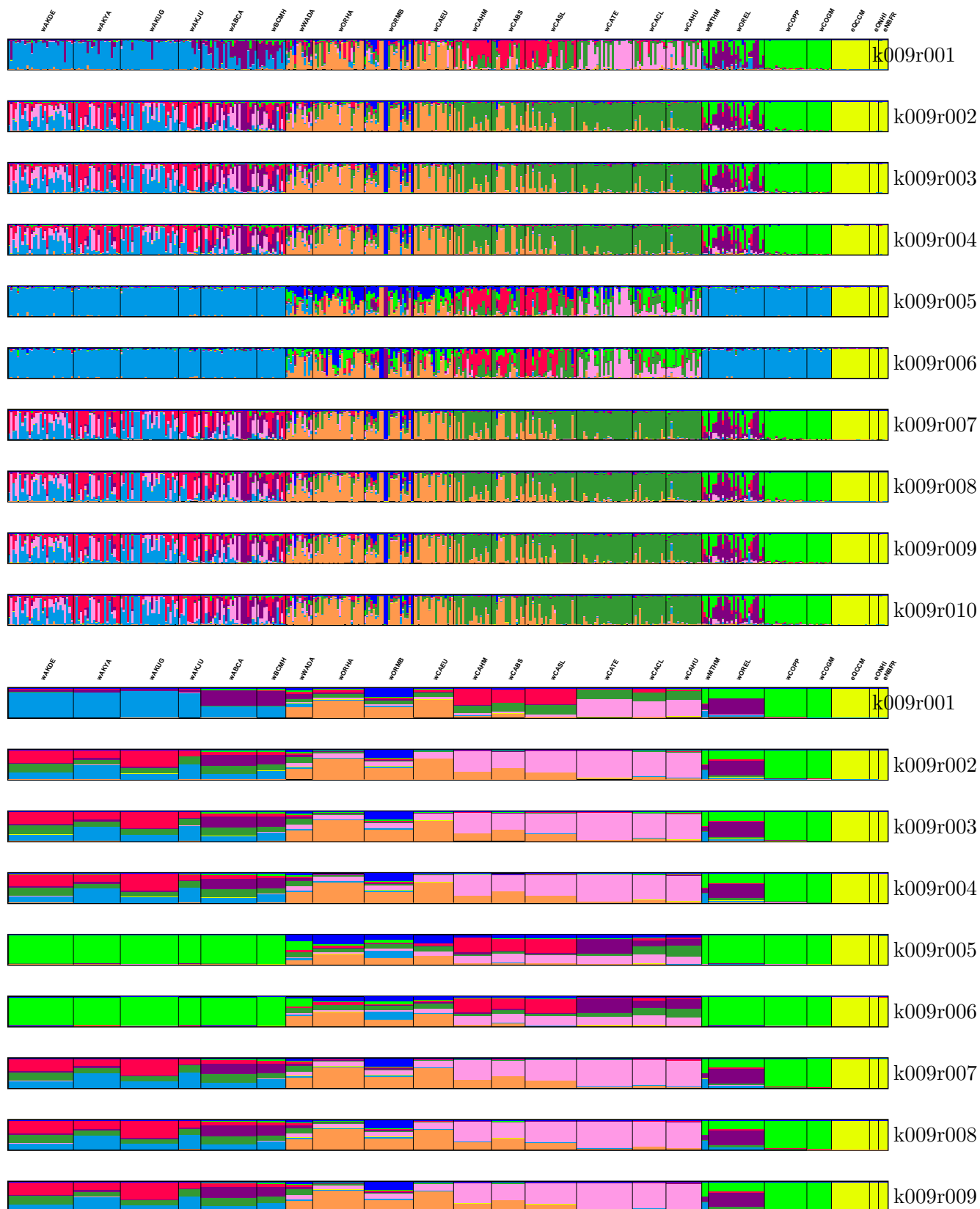


Distruct Plots at  $K = 7$ .





Distruct Plots at  $K = 8$ .



Distruct Plots at  $K = 9$ .